

#19

1646

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/114,844B

DATE: 02/20/2001
 TIME: 16:25:58

Input Set : A:\P1129R1 (REVISED).txt
 Output Set: N:\CRF3\02202001\I114844B.raw

ENTERED

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MAR 02 2001

TECH CENTER 1600/2900

3 <110> APPLICANT: Ashkenazi, Avi J.
 4 Gurney, Austin
 6 <120> TITLE OF INVENTION: RTD Receptor
 8 <130> FILE REFERENCE: P1129R1 (REVISED)
 10 <140> CURRENT APPLICATION NUMBER: US 09/114,844B
 11 <141> CURRENT FILING DATE: 1998-07-14
 13 <150> PRIOR APPLICATION NUMBER: US 60/056,974
 14 <151> PRIOR FILING DATE: 1997-08-26
 16 <160> NUMBER OF SEQ ID NOS: 10
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 386
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Homo sapiens
 23 <220> FEATURE:
 24 <221> NAME/KEY: unsure
 25 <222> LOCATION: 310
 26 <223> OTHER INFORMATION: Xaa may be serine or leucine
 28 <400> SEQUENCE: 1
 29 Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala Ser Ser Ala Arg
 30 1 5 10 15
 32 Ala Gly Arg Tyr Pro Gly Ala Arg Thr Ala Ser Gly Thr Arg Pro
 33 20 25 30
 35 Trp Leu Leu Asp Pro Lys Ile Leu Lys Phe Val Val Phe Ile Val
 36 35 40 45
 38 Ala Val Leu Leu Pro Val Arg Val Asp Ser Ala Thr Ile Pro Arg
 39 50 55 60
 41 Gln Asp Glu Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg
 42 65 70 75
 44 Arg Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg Ser
 45 80 85 90
 47 Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly Val Asp Tyr
 48 95 100 105
 50 Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys Leu Leu Cys Thr Val
 51 110 115 120
 53 Cys Lys Ser Gly Gln Thr Asn Lys Ser Ser Cys Thr Thr Thr Arg
 54 125 130 135
 56 Asp Thr Val Cys Gln Cys Glu Lys Gly Ser Phe Gln Asp Lys Asn
 57 140 145 150
 59 Ser Pro Glu Met Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly
 60 155 160 165
 62 Met Val Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys
 63 170 175 180
 65 Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro Ala Ala
 66 185 190 195
 68 Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu Ala Ser Pro Tyr
 69 200 205 210
 71 His Tyr Leu Ile Ile Ile Val Val Leu Val Ile Ile Leu Ala Val

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72 215 220 225
 74 Val Val Val Gly Phe Ser Cys Arg Lys Lys Phe Ile Ser Tyr Leu
 75 230 235 240
 77 Lys Gly Ile Cys Ser Gly Gly Gly Gly Gly Pro Glu Arg Val His
 78 245 250 255
 80 Arg Val Leu Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly
 81 260 265 270
 83 Ala Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr Leu
 84 275 280 285
 86 Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly Gln Glu Leu
 87 290 295 300
 89 Ala Glu Leu Thr Gly Val Thr Val Glu Xaa Pro Glu Glu Pro Gln
 90 305 310 315
 92 Arg Leu Leu Glu Gln Ala Glu Ala Glu Gly Cys Gln Arg Arg Arg
 93 320 325 330
 95 Leu Leu Val Pro Val Asn Asp Ala Asp Ser Ala Asp Ile Ser Thr
 96 335 340 345
 98 Leu Leu Asp Ala Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu
 99 350 355 360
 101 Thr Ile Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu
 102 365 370 375
 104 Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu
 105 380 385
 107 <210> SEQ ID NO: 2
 108 <211> LENGTH: 2082
 109 <212> TYPE: DNA
 110 <213> ORGANISM: Homo sapiens
 112 <220> FEATURE:
 113 <221> NAME/KEY: unsure
 114 <222> LOCATION: 1085
 115 <223> OTHER INFORMATION: Y may be cytosine, thymine or uracil
 117 <400> SEQUENCE: 2
 118 ccaactgcac ctcggttcta tcgattgaat tccccgggga tcctctagag 50
 120 atccctcgac ctcgaccac gcgtccggaa cctttgcacg cgcacaaact 100
 122 acggggacga tttctgattg atttttggcg ctttcgatcc accctctctc 150
 124 cttctc atg gga ctt tgg gga caa agc gtc ccg acc gcc 189
 125 Met Gly Leu Trp Gly Gln Ser Val Pro Thr Ala
 126 1 5 10
 128 tcg agc gct cga gca ggg cgc tat cca gga gcc agg aca 228
 129 Ser Ser Ala Arg Ala Gly Arg Tyr Pro Gly Ala Arg Thr
 130 15 20
 132 gcg tcg gga acc aga cca tgg ctc ctg gac ccc aag atc 267
 133 Ala Ser Gly Thr Arg Pro Trp Leu Leu Asp Pro Lys Ile
 134 25 30 35
 136 ctt aag ttc gtc gtc ttc atc gtc gcg gtt ctg ctg ccg 306
 137 Leu Lys Phe Val Val Phe Ile Val Ala Val Leu Leu Pro
 138 40 45 50
 140 gtc cgg gtt gac tct gcc acc atc ccc cgg cag gac gaa 345
 141 Val Arg Val Asp Ser Ala Thr Ile Pro Arg Gln Asp Glu

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142          55          60
144 gtt ccc cag cag aca gtg gcc cca cag caa cag agg cgc 384
145 Val Pro Gln Gln Thr Val Ala Pro Gln Gln Gln Arg Arg
146      65          70          75
148 agc ctc aag gag gag gag tgt cca gca gga tct cat aga 423
149 Ser Leu Lys Glu Glu Glu Cys Pro Ala Gly Ser His Arg
150          80          85
152 tca gaa tat act gga gcc tgt aac ccg tgc aca gag ggt 462
153 Ser Glu Tyr Thr Gly Ala Cys Asn Pro Cys Thr Glu Gly
154  90          95          100
156 gtg gat tac acc att gct tcc aac aat ttg cct tct tgc 501
157 Val Asp Tyr Thr Ile Ala Ser Asn Asn Leu Pro Ser Cys
158      105          110          115
160 ctg cta tgt aca gtt tgt aaa tca ggt caa aca aat aaa 540
161 Leu Leu Cys Thr Val Cys Lys Ser Gly Gln Thr Asn Lys
162          120          125
164 agt tcc tgt acc acg acc aga gac acc gtg tgt cag tgt 579
165 Ser Ser Cys Thr Thr Thr Arg Asp Thr Val Cys Gln Cys
166      130          135          140
168 gaa aaa gga agc ttc cag gat aaa aac tcc cct gag atg 618
169 Glu Lys Gly Ser Phe Gln Asp Lys Asn Ser Pro Glu Met
170          145          150
172 tgc cgg acg tgt aga aca ggg tgt ccc aga ggg atg gtc 657
173 Cys Arg Thr Cys Arg Thr Gly Cys Pro Arg Gly Met Val
174      155          160          165
176 aag gtc agt aat tgt acg ccc cgg agt gac atc aag tgc 696
177 Lys Val Ser Asn Cys Thr Pro Arg Ser Asp Ile Lys Cys
178          170          175          180
180 aaa aat gaa tca gct gcc agt tcc act ggg aaa acc cca 735
181 Lys Asn Glu Ser Ala Ala Ser Ser Thr Gly Lys Thr Pro
182          185          190
184 gca gcg gag gag aca gtg acc acc atc ctg ggg atg ctt 774
185 Ala Ala Glu Glu Thr Val Thr Thr Ile Leu Gly Met Leu
186      195          200          205
188 gcc tct ccc tat cac tac ctt atc atc ata gtg gtt tta 813
189 Ala Ser Pro Tyr His Tyr Leu Ile Ile Ile Val Val Leu
190          210          215
192 gtc atc att tta gct gtg gtt gtg gtt ggc ttt tca tgt 852
193 Val Ile Ile Leu Ala Val Val Val Val Gly Phe Ser Cys
194      220          225          230
196 cgg aag aaa ttc att tct tac ctc aaa ggc atc tgc tca 891
197 Arg Lys Lys Phe Ile Ser Tyr Leu Lys Gly Ile Cys Ser
198          235          240          245
200 ggt ggt gga gga ggt ccc gaa cgt gtg cac aga gtc ctt 930
201 Gly Gly Gly Gly Gly Pro Glu Arg Val His Arg Val Leu
202          250          255
204 ttc cgg cgg cgt tca tgt cct tca cga gtt cct ggg gcg 969
205 Phe Arg Arg Arg Ser Cys Pro Ser Arg Val Pro Gly Ala
206      260          265          270

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208 gag gac aat gcc cgc aac gag acc ctg agt aac aga tac 1008
 209 Glu Asp Asn Ala Arg Asn Glu Thr Leu Ser Asn Arg Tyr
 210 275 280
 212 ttg cag ccc acc cag gtc tct gag cag gaa atc caa ggt 1047
 213 Leu Gln Pro Thr Gln Val Ser Glu Gln Glu Ile Gln Gly
 214 285 290 295
 216 cag gag ctg gca gag cta aca ggt gtg act gta gag tyg 1086
 217 Gln Glu Leu Ala Glu Leu Thr Gly Val Thr Val Glu Xaa
 218 300 305 310
 220 cca gag gag cca cag cgt ctg ctg gaa cag gca gaa gct 1125
 221 Pro Glu Glu Pro Gln Arg Leu Leu Glu Gln Ala Glu Ala
 222 315 320
 224 gaa ggg tgt cag agg agg agg ctg ctg gtt cca gtg aat 1164
 225 Glu Gly Cys Gln Arg Arg Arg Leu Leu Val Pro Val Asn
 226 325 330 335
 228 gac gct gac tcc gct gac atc agc acc ttg ctg gat gcc 1203
 229 Asp Ala Asp Ser Ala Asp Ile Ser Thr Leu Leu Asp Ala
 230 340 345
 232 tcg gca aca ctg gaa gaa gga cat gca aag gaa aca att 1242
 233 Ser Ala Thr Leu Glu Glu Gly His Ala Lys Glu Thr Ile
 234 350 355 360
 236 cag gac caa ctg gtg ggc tcc gaa aag ctc ttt tat gaa 1281
 237 Gln Asp Gln Leu Val Gly Ser Glu Lys Leu Phe Tyr Glu
 238 365 370 375
 240 gaa gat gag gca ggc tct gct acg tcc tgc ctg tgaaag 1320
 241 Glu Asp Glu Ala Gly Ser Ala Thr Ser Cys Leu
 242 380 385
 244 aatctcttca ggaaccaga gcttccctca tttacctttt ctctacaaa 1370
 246 gggaagcagc ctggaagaaa cagtccagta cttgacocat gccccacaa 1420
 248 actctactat ccaatatggg gcagcttacc aatgggtccta gaactttgtt 1470
 250 aacgcacttg gagtaatttt tatgaaatac tgcgtgtgat aagcaaacgg 1520
 252 gagaaattta tatcagattc ttggctgcat agttatacga ttgtgtatta 1570
 254 agggctgctt taggccacat gcggtggctc atgcctgtaa tcccagcact 1620
 256 ttgataggct gaggcagggt gattgcttga gctcgggagt ttgagaccag 1670
 258 cctcatcaac acagtgaac tccatctcaa tttaaaaga aaaaaagtgg 1720
 260 ttttaggatg tcattctttg cagttcttca tcatgagaca agtctttttt 1770
 262 tctgcttctt atattgcaag ctccatctct actggtgtgt gcatttaattg 1820
 264 acatctaact acagatgccg cacagccaca atgctttgcc ttatagtttt 1870
 266 ttaactttag aacgggatta tcttgttatt acctgtattt tcagtttcgg 1920
 268 atatttttga cttaatgatg agattatcaa gacgtacccc tatgctaagt 1970
 270 catgagcata tggacttacg agggttcgac ttagagtttt gagctttaag 2020
 272 ataggattat tgggggctta cccccacctt aattagaaga aacattttat 2070
 274 attgctttac ta 2082
 276 <210> SEQ ID NO: 3
 277 <211> LENGTH: 50
 278 <212> TYPE: DNA
 279 <213> ORGANISM: Artificial sequence
 281 <220> FEATURE:
 282 <223> OTHER INFORMATION: Sequence is synthesized.

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284 <400> SEQUENCE: 3
285   cataaaagt cctgcacccat gaccagagac acagtgtgtc agtgtaaaga 50
287 <210> SEQ ID NO: 4
288 <211> LENGTH: 24
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: Sequence is synthesized.
295 <400> SEQUENCE: 4
296   cttcaggaaa ccagagcttc cctc 24
298 <210> SEQ ID NO: 5
299 <211> LENGTH: 24
300 <212> TYPE: DNA
301 <213> ORGANISM: Artificial sequence
303 <220> FEATURE:
304 <223> OTHER INFORMATION: Sequence is synthesized.
306 <400> SEQUENCE: 5
307   ttctcccggtt tgcttatcac acgc 24
309 <210> SEQ ID NO: 6
310 <211> LENGTH: 191
311 <212> TYPE: PRT
312 <213> ORGANISM: Homo sapiens
314 <400> SEQUENCE: 6
315   Gly Arg Gly Ala Leu Pro Thr Ser Met Gly Gln His Gly Pro Ser
316       1             5             10             15
318   Ala Arg Ala Arg Ala Gly Arg Ala Pro Gly Pro Arg Pro Ala Arg
319               20             25             30
321   Glu Ala Ser Pro Arg Leu Arg Val His Lys Thr Phe Lys Phe Val
322               35             40             45
324   Val Val Gly Val Leu Leu Gln Val Val Pro Ser Ser Ala Ala Thr
325               50             55             60
327   Ile Lys Leu His Asp Gln Ser Ile Gly Thr Gln Gln Trp Glu His
328               65             70             75
330   Ser Pro Leu Gly Glu Leu Cys Pro Pro Gly Ser His Arg Ser Glu
331               80             85             90
333   Arg Pro Gly Ala Cys Asn Arg Cys Thr Glu Gly Val Gly Tyr Thr
334               95            100            105
336   Asn Ala Ser Asn Asn Leu Phe Ala Cys Leu Pro Cys Thr Ala Cys
337               110            115            120
339   Lys Ser Asp Glu Glu Glu Arg Ser Pro Cys Thr Thr Thr Arg Asn
340               125            130            135
342   Thr Ala Cys Gln Cys Lys Pro Gly Thr Phe Arg Asn Asp Asn Ser
343               140            145            150
345   Ala Glu Met Cys Arg Lys Cys Ser Thr Gly Cys Pro Arg Gly Met
346               155            160            165
348   Val Lys Val Lys Asp Cys Thr Pro Trp Ser Asp Ile Glu Cys Val
349               170            175            180
351   His Lys Glu Ser Gly Asn Gly His Asn Ile Trp
352               185            190

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VERIFICATION SUMMARY
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Input Set : A:\P1129R1 (REVISED).txt
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L:89 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2